
WIRE
***** (TW)
Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Feb 6 12:26:06 1997; Maspar time 21.99 Seconds
632.952 Million cell updates/sec
Tabular output not generated.

File: >US-08-468-011-2
Description: (1-541) from US08468011.pep
Accession: 4132
Sequence: 1 MAWLGLASLHWGWLMLGSLC.....DDLMEKPSRPMESNPDTEG 541

Scoring table: PAM 150
Gap 11
Searched: 82182 seqs, 25727515 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann
14:unrev

Statistics: Mean 48.841; Variance 115.276; scale 0.424
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Description	Pred. No.
1	3721	90.1	parathyroid hormone	0.00e+00
2	2051	49.6	parathyroid hormone	0.00e+00
3	1966	47.6	parathyroid hormone	0.00e+00
4	1943	47.0	parathyroid hormone	0.00e+00
5	1942	47.0	parathyroid hormone	0.00e+00
6	1931	46.7	parathyroid hormone	0.00e+00
7	1026	24.8	parathyroid hormone	0.00e+00
8	1003	24.3	parathyroid hormone	0.00e+00
9	990	24.0	parathyroid hormone	0.00e+00
10	983	23.8	parathyroid hormone	0.00e+00
11	975	23.6	parathyroid hormone	0.00e+00
12	964	23.3	parathyroid hormone	0.00e+00
13	907	22.0	parathyroid hormone	0.00e+00
14	900	21.8	parathyroid hormone	0.00e+00
15	877	21.2	parathyroid hormone	0.00e+00
16	863	20.9	parathyroid hormone	0.00e+00
17	845	20.5	parathyroid hormone	0.00e+00
18	843	20.4	parathyroid hormone	0.00e+00
19	825	20.0	parathyroid hormone	0.00e+00
20	818	19.8	parathyroid hormone	0.00e+00
21	816	19.7	parathyroid hormone	0.00e+00

22	807	19.5	462 12	JC2462	gastric inhibitory p	2.31e-112
23	793	19.2	467 12	JN0616	pituitary adenylate	6.18e-110
24	782	18.9	490 11	S34486	calcitonin receptor	4.97e-108
25	780	18.9	525 11	JN0902	pituitary adenylate	1.10e-107
26	762	18.4	423 11	A45367	growth hormone-relea	1.43e-104
27	757	18.3	423 11	A45363	growth hormone-relea	1.04e-103
28	754	18.2	516 12	S33747	calcitonin receptor	3.45e-103
29	737	17.8	474 11	S44209	calcitonin receptor	2.96e-100
30	711	17.2	423 12	S29753	growth hormone-relea	8.89e-96
31	704	17.0	479 12	S33746	calcitonin receptor	1.42e-94
32	653	15.8	482 12	A39285	calcitonin receptor	7.88e-86
33	644	15.6	461 11	JC2477	calcitonin receptor	2.72e-84
34	595	14.4	415 11	S39534	corticotropin-relea	5.98e-76
35	591	14.3	415 12	S39535	corticotropin-relea	2.85e-75
36	584	14.1	430 12	A56726	corticotropin recep	4.38e-74
37	542	13.1	494 14	S39063	pituitary adenylate	5.42e-67
38	538	13.0	495 12	S36114	pituitary adenylate	2.55e-66
39	538	13.0	495 12	S39061	pituitary adenylate	2.55e-66
40	538	13.0	495 12	A48204	pituitary adenylate	2.55e-66
41	538	13.0	523 14	S39060	pituitary adenylate	2.55e-66
42	535	12.9	381 12	S33449	pituitary adenylate	8.15e-66
43	533	12.9	513 14	A47631	pituitary adenylate	1.77e-65
44	456	11.0	464 12	S29754	growth hormone-relea	1.23e-52
45	270	6.5	206 10	S23242	hypothetical protein	7.35e-23

ALIGNMENTS

RESULT 1
ENTRY A57519 #type complete
TITLE parathyroid hormone receptor 2 precursor - human
ALTERNATE_NAMES PTH2 receptor
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change
ACCESSIONS A57519
REFERENCE A57519
AUTHORS Usdin, T.B.; Gruber, C.; Bonner, T.I.
#journal J. Biol. Chem. (1995) 270:15455-15458
#title Identification and functional expression of a receptor
selectively recognizing parathyroid hormone, the PTH2
receptor.
#accession A57519
#status preliminary
#molecule_type mRNA
#residues 1-550 #label USD
#cross-references GB:U25128
#note nucleotide sequence not given
KEYWORDS hormone receptor
SUMMARY #length 550 #molecular-weight 62235 #checksum 2724

6/30/95

Query Match	90.1%	Score 3721; DB 11; Length 550;
Best Local Similarity	91.5%;	Pred. No. 0.00e+00;
Matches	496; Conservative 18; Mismatches 26; Indels 2; Gaps 2;	
Db	1	magigaslhvqwlmgscllaragldsgdtiteeqivlvkavqcelnitaqlqege 60
Qy	1	MAWLGLASLHWGWLMLGSLC...DDLMEKPSRPMESNPDTEG 541
Db	61	gncfpewdglcwpgrtgvgkisavpcppiyidfnhkgvafchncpntgdfmshlnkwa 120
Qy	61	GNCFPWDGLCWPGRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKWA 120
Db	121	nysdclrfiqpdislgkqfefferlymyvtvgysifsgslavalliglyfrlhrtrnyih 180
Qy	121	NYSCLRFQLPQDISLGKQFEFRLYMYVTGYSISFGSLAVAILIIGYFRRLHCTRNIH 180
Db	181	mhlvsvfmlratsfvkdrvvahigvkeleslmqddpqnsciatssvdksgyigckia 240
Qy	181	MHLVSVFMLRATSFVKDRVVHAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
Db	241	vmfiyflatnnywllveqlylhnlfvaffsdtkylvgflligwgfpaafvaavarat 300
Qy	241	VMFIYFLATNYYWLLVEQLYLHNLFVAFFSDTKYLVGFIIGWGFPAAFVAAVARAT 300


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Query Match      23.8%; Score 983; DB 12; Length 495;
Best Local Similarity 40.3%; Pred. No. 4.59e-143;
Matches 182; Conservative 91; Mismatches 107; Indels 42; Gaps 27;

Db 84 qc-le-eaqlenetigskmwnltcwpatprgvgvvlacplkflfssiqgrnvs-rsc 140
QY 47 QCELNITAQLQEGEGNCPEWDGLICWPGVGVKISAVPCPP-Y-IYDFNH-KGVAFRHC 103
Db 141 tdeg-wt--h-le-p-gpytlaclddaasldseqtmqfsgvsktytgyglslatll 194
QY 104 NPNGTDFMHSLNKTWANY-DC-LRFLQPDISIGKQFCERLYVMYTVGYSISFGSLAV 161
Db 195 atailsfrklhctnrnylhmlfslfslraaavf-----i--kdl-alf--dsge- 239
QY 162 AILLIGFRRRLHCTNRNIHMLFVFSFMRATSFVKORVVHAHIGVKELESIMQDDPON 221
Db 240 s-dqcs-egs--vgckaamffqvcvmanffllveglytlllavaffserkyfwyil 295
QY 222 SIATSVDSKQSYIGCKTAVVMFIVFLATNYWILVEGLYLHNLIFVAFSFTKYLWGFIL 281
Db 296 igwvpsftmvtiarihfedyllrcwdtinslwlkpgiltsilvnlflficilr 355
QY 282 IGWGFPAFVAAMAVARATLAD-A--RCWELSGADIKWIYQAPILAAIGLNFILFLNTR 338
Db 356 illqklrppdirksds-pysrlarstlllplfgvhyimaffpndfnp---evkmvfe 411
QY 339 VLATKINETNAVGHDTKQYKRLAKSLVLVLVFGVHYIVFVCLPHSFTGLGWELRMHCE 398
Db 412 lvvsgfgfvvaallycflngevqeqlrkrwhlqglvwn 453
QY 399 LFFNSFGFFVSIYCYCNGEVQAEVKMWSRWNL-SV-DWK 438

RESULT 11
ENTRY      S16319      #type complete
TITLE      secretin receptor - rat
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995

ACCESSIONS S16319
REFERENCE   Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.;
#authors   Takahashi, K.; Nagata, S.
#journal   EMBO J. (1991) 10:1635-1641
#title     Molecular cloning and expression of a cDNA encoding the
#accession secretin receptor.
#status     preliminary
#molecule_type mRNA
#residues   1-449 #label ISH
#cross-references EMBL:X59132
#length 449 #molecular-weight 51234 #checksum 33

Query Match      23.6%; Score 975; DB 12; Length 449;
Best Local Similarity 40.7%; Pred. No. 1.16e-141;
Matches 184; Conservative 97; Mismatches 95; Indels 32; Gaps 16;

Db 61 etasgcglwdmcsppaspartveqcpkflmlsnknsgslfrnctqdg-ws--etfp 117
QY 58 EGEKNCPEWDGLICWPGVGVKISAVPCPPYIYDFNHK-GVAFRHCNPGTDFMHSLN 116
Db 118 r--pdla-cgvnlnnsfnerrhayllklkmvtyvgyssslamllvalsfrlhcrr 174
QY 117 KTWANYSDCLRFQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTR 176
Db 175 nyihmhlvsvflralsnfikd---a---v-----lfssddvtyc-da---hk---vvc 215
QY 177 NYIHHHLFVSPMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIATSVDSKQYIGC 236
Db 216 klvmiffqycimanyavllveglylhtllaisffserkylqafvllgwgsfaifvalwai 275
QY 175 NYIHHHLFVSPMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIATSVDSKQYIGC 236

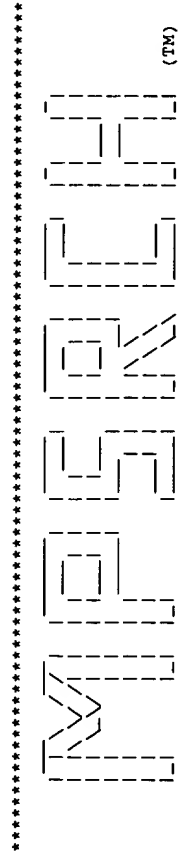
Query Match      23.3%; Score 964; DB 14; Length 440;
Best Local Similarity 42.5%; Pred. No. 9.80e-140;
Matches 157; Conservative 87; Mismatches 93; Indels 32; Gaps 16;

Db 70 wdniscwpsvprgmvevecpfrflmtrngslfrnctqdg-ws--etfpr--pnlac 123
QY 67 WDGLICWPGVGVKISAVPCPPYIYDF-NHKGVAFRHCNPGTDFMHSLNKTWANYSDC 125
Db 124 avnvndssnekrhsyllkikmvtvgyssslvmlvalgilcafrlhcrrnyihmhlv 183
QY 126 LRFLQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTNRNYHMLFV 185
Db 184 sflralsnfikd---a---v-----lfssddvtyc-da---hra---gcklvmvlfqy 224
QY 186 SFMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIATSVDSKQYIGCKTAVVMFY 245
Db 225 clmanysvllveglylhtllaisffserkylqafvgsfaifvalwaiarhlfedvg 284
QY 246 FLATNYWILVEGLYLHNLIFVAFSFTKYLWGFILIGWGFPAFVAAMAVARATLADAR 305
Db 285 cwdinasaiwvrgpvalsilinfilnrlmrlkrtqetrgnvs-hykrslars 343
QY 306 CWELSA-GDIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYKRLAKS 364
Db 344 tlllplfgthyivfa-fspe-dam--eiqlffellalasfgqlvavlycflngevqlv 399
QY 365 TLVLVLVFGVHYIVFVCLPHSFTGLGWELRMHCELFNSFQGFVSIYCYCNGEQVAEV 424
Db 400 qkkwqgwhl 408
QY 425 KMWWSRWNL 433

RESULT 13
ENTRY      JU0185      #type complete
TITLE      PACAP receptor subtype 3 - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
23-Mar-1995

ACCESSIONS JU0185
```

Db	95	dg-ws--etfpd-fid-a-c-gyndpe-deskitfylvkaiylglgysvslmstltgsii	146
QY	106	NGTWDFMHSLNKTWANSYDCLRFQPDISIGKQEFCELYVMYTVGYSFSGSLAVAIL	165
Db	147	iclfkrkthcrnyihnlfnlraismraivskvdslysssgt--lrc--hdqp-----	195
QY	166	IGVFRRLHCRNTHHMLFVSFMRLETSIFVKDVRVHAHIGVKELSLIMQDDPQNSIEA	225
Db	196	-g---s-wvgckislsvffycimafnyllveglylhtll-vailbpsrcfiaylligwg	249
QY	226	TSVDKSOYIGCKIAVVMYFVFLATNYWILVEGLYLHNLIFFVAFFSDTKYLMGFI	285
Db	250	ipsvcigawiatrlsldetgcwdtndhsipwvwrmpilisivvnfalfisvtrllqkl	309
QY	286	FPAAFVAAMAVARATLADARCWLSAGDIKW-IYQAPILAAAGLNLFLNTVRVLATKI	344
Db	310	-tspdvggndqsgykrklakstlllplfgvhyvmfaafpigriss-tyql-lf-elcvgsf	365
QY	345	WETNVAUGHDRKQYRKLAJSTLVLVLFVGFVHYHIVFVCLPHSFITGLGWEIMHCELF	404
Db	366	qglvvavlycflnsevcqelkrw	389
QY	405	QGFEVSIYCYCNGEYQAEVKMW	428
RESULT	15		
ENTRY	JC2463	#type complete	
TITLE	vasoactive intestinal peptide receptor - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 05-Jan-1996		
ACCESSIONS	JC2463		
REFERENCE	JC2463		
#authors	Svoboda, M.; Tastenoj, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbroeck, M.; Robberecht, P.		
#journal	Biochem. Biophys. Res. Commun. (1994) 205:1617-1624		
#title	Molecular cloning and functional characterization of a human VIP receptor from SUP-T1 lymphoblasts.		
#accession	JC2463		
#molecule_type	mRNA		
#residues	1-438 ##label SVO		
#cross-references	GB:L36566		
#experimental_source	SUP-T1 lymphoblast cell line		
KEYWORDS	glycoprotein; receptor; transmembrane protein		
FEATURE			
130-150	#domain transmembrane #status predicted #label TM1\		
160-179	#domain transmembrane #status predicted #label TM2\		
206-228	#domain transmembrane #status predicted #label TM3\		
241-262	#domain transmembrane #status predicted #label TM4\		
282-304	#domain transmembrane #status predicted #label TM5\		
329-349	#domain transmembrane #status predicted #label TM6\		
361-384	#domain transmembrane #status predicted #label TM7\		
58,88,92	#binding_site carbohydrate (Asn) (covalent) #status predicted		
SUMMARY	#length 438 #molecular-weight 49503 #checksum 8054		
Query Match	21.2%; Score 877; DB 12; Length 438;		
Best Local Similarity	36.3%; Pred. No. 1.56e-124;		
Matches	153; Conservative 111; Mismatches 121; Indels 36; Gaps		
Db	4	llppalltcwlapvnsipcefrhlieqeeetkctel-lrsg-tekhkacagvwdnic	61
QY	15	MLGSCLLARRAQLSDGTITIEQIVL-VLKAKVQC-ELNITAQLOGEGNCPEWDLGIC	72
Db	62	wrpanvgetvpcpkvfnsfnyskagniskntsdg-ws--etfpd-fvd-a-c-gysdp	114
QY	73	WPRGTGKISAVPCPYIYDFNHKGVAF-RHCNPNGTDFMHSLNKTWANSYDCLRFLOP	131
Db	115	e-deskitfylvkaiylglgysvslmstlsglclfrklbctnrnyihnlfnlslfira	173
QY	132	DISIGKQEFCELYVMYTVGYSFSGSLAVAILIIGYFRLLHCTRNYIHMHFVSFMR	191



(TM)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Feb 6 12:25:21 1997; MasPar time 17.41 Seconds
Tabular output not generated. 575.852 Million cell updates/sec

>US-08-468-011-2
(1-541) from US08468011.pep
Sequence: 1 MAWLGAHLVWGWLMLGSL.....DDLMEKPSRPMESNPDTG 541

Scoring table: PAM 150
Gap 11

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 50.887; Variance 95.964; scale 0.530

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3721	90.1	550	7	PTR2_HUMAN PARATHYROID HORMONE R	0.00e+00
2	2057	49.8	585	7	PTRR_DIDMA PARATHYROID HORMONE/P	0.00e+00
3	1966	47.6	591	7	PTRR_RAT PARATHYROID HORMONE/P	0.00e+00
4	1943	47.0	591	7	PTRR_MOUSE PARATHYROID HORMONE/P	0.00e+00
5	1942	47.0	593	7	PTRR_HUMAN PARATHYROID HORMONE/P	0.00e+00
6	1026	24.8	459	9	VIPR_RAT VASOACTIVE INTESTINAL	9.02e-188
7	1003	24.3	459	9	VIPR_HUMAN VASOACTIVE INTESTINAL	9.32e-183
8	975	23.6	449	8	SCRC_RAT SECRETIN RECEPTOR PRE	1.34e-176
9	964	23.3	440	8	SCRC_HUMAN SECRETIN RECEPTOR PRE	3.40e-174
10	907	22.0	437	9	VIPS_MOUSE VASOACTIVE INTESTINAL	9.38e-162
11	900	21.8	437	9	VIPS_RAT VASOACTIVE INTESTINAL	3.14e-160
12	877	21.2	438	9	VIPS_HUMAN VASOACTIVE INTESTINAL	3.18e-155
13	863	20.9	463	4	GLPR_RAT GLUCAGON-LIKE PEPTIDE	3.51e-152
14	845	20.5	477	4	GLR_RAT GLUCAGON RECEPTOR PRE	2.84e-148
15	845	20.5	485	4	GLR_HUMAN GLUCAGON RECEPTOR PRE	2.84e-148
16	828	20.0	463	4	GLPR_HUMAN GLUCAGON-LIKE PEPTIDE	1.38e-144
17	807	19.5	462	4	GIPR_HUMAN GASTRIC INHIBITORY PO	4.86e-140
18	780	18.9	468	6	PACR_HUMAN PITUITARY ADENYLATE C	3.32e-134
19	782	18.9	490	2	CALR_HUMAN CALCITONIN RECEPTOR P	1.23e-134
20	772	18.7	466	4	GIPR_HUMAN GASTRIC INHIBITORY PO	1.77e-132
21	757	18.3	423	4	GRFR_HUMAN GROWTH HORMONE-RELEAS	3.03e-129
22	753	18.2	451	4	GRFR_PIG GROWTH HORMONE-RELEAS	2.20e-128

23	754	18.2	516	2	CLRB_RAT CALCITONIN RECEPTOR B	1.34e-128
24	745	18.0	455	4	GIPR_RAT GASTRIC INHIBITORY PO	1.16e-126
25	711	17.2	423	4	GRFR_MOUSE GROWTH HORMONE-RELEAS	2.34e-119
26	704	17.0	479	2	CLRA_RAT CALCITONIN RECEPTOR A	7.42e-118
27	653	15.8	444	2	CRFR_HUMAN CORTICOTROPIN RELEASI	5.88e-107
28	653	15.8	482	2	CALR_PIG CALCITONIN RECEPTOR P	5.88e-107
29	591	14.3	411	2	CFR2_RAT CORTICOTROPIN RELEASI	8.43e-94
30	591	14.3	415	2	CRFR_MOUSE CORTICOTROPIN RELEASI	8.43e-94
31	589	14.3	415	2	CRFR_RAT CORTICOTROPIN RELEASI	2.23e-93
32	538	13.0	523	6	PACR_RAT PITUITARY ADENYLATE C	1.19e-82
33	449	10.9	464	4	GRFR_RAT GROWTH HORMONE-RELEAS	3.46e-64
34	350	8.5	395	3	DIHR_MANSE DIURETIC HORMONE RECE	2.48e-44
35	310	7.5	522	10	YOW3_CAEEL PROBABLE G PROTEIN-CO	2.48e-36
36	192	4.6	742	2	CD97_HUMAN LEUCOCYTE ANTIGEN CD9	1.64e-14
37	118	2.9	420	5	MLIC_XENLA MELATONIN RECEPTOR TY	7.29e-03
38	119	2.9	428	8	SSR3_MOUSE SOMATOSTATIN RECEPTOR	5.31e-03
39	121	2.9	748	5	JSBI_TRINI BASIC JUVENILE HORMON	2.91e-02
40	112	2.7	384	6	NK2R_BOVIN SUBSTANCE-K RECEPTOR	4.69e-02
41	107	2.6	154	9	VG51_HSVI1 HYPOTHETICAL GENE 51	2.10e-01
42	106	2.6	498	1	ADT_RICPR ADP,ATP CARRIER PROTE	2.81e-01
43	105	2.5	328	10	YHJD_ERWCH HYPOTHETICAL 36.0 KD	3.76e-01
44	105	2.5	393	10	YWCF_BAGSU HYPOTHETICAL 43.3 KD	3.76e-01
45	105	2.5	423	4	GCRC_MOUSE PROBABLE G PROTEIN-CO	3.76e-01

ALIGNMENTS

RESULT	1	PTR2_HUMAN	STANDARD;	PRT;	550 AA.
AC	P49190;				
DT	01-FEB-1996 (REL. 33, CREATED)				
DT	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)				
DE	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).				
GN	PTH2.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUETHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN;				
RX	MEDLINE; 95318121.				
RA	USJN T.B., GRUBER C., BONNER T.I.;				
RL	J. BIOL. CHEM. 270:15455-15458(1995).				
CC	-!- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL CYCLASE.				
CC	-!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.				
CC	-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL: U25128; G887967; -				
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.				
FT	SIGNAL	1	24		POTENTIAL.
FT	CHAIN	25	550		PARATHYROID HORMONE RECEPTOR.
FT	DOMAIN	27	145		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	146	169		1 (POTENTIAL).
FT	DOMAIN	170	176		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	177	196		2 (POTENTIAL).
FT	DOMAIN	197	237		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	238	260		3 (POTENTIAL).
FT	DOMAIN	261	275		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	276	297		4 (POTENTIAL).
FT	DOMAIN	298	316		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	317	337		5 (POTENTIAL).
FT	DOMAIN	338	364		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	365	383		6 (POTENTIAL).
FT	DOMAIN	384	394		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	395	417		7 (POTENTIAL).
FT	DOMAIN	418	550		CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	51	51		POTENTIAL.
FT	CARBOHYD	106	106		POTENTIAL.
FT	CARBOHYD	116	116		POTENTIAL.
FT	CARBOHYD	121	121		POTENTIAL.
SQ	SEQUENCE	550 AA;	62235 MW;		DD481286 CRC32;


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123 SDCLRLQPDISIGKQECERLYVMTYVGYISGSLAVAILIIGYFRLHCTRNHYHM 182
226 mflsfmlraasifvkdavlysgftldeaelrteehhlaqvppppaaavagcgvav 285
193 LFSFMLRATISIFKDRVYVHAHIGVKELESIMOD-DPQNSIEATSVDKS-QYIGCKIAV 240
286 tfflyflatnywllvegilyhslfmaffsekkyllwgtlfgwglpavfvavvgrat 345
241 VMFYFLATNYWLLVEGLYLHNLIFVAFSDTKYLGWFLIIGWGFPAFVAANAVARAT 300
346 lantgcwldssghkwiqvillasvlnfilnirvlatklretnagrcdtrqyrk 405
301 LADARCWELSAGDKIWKIYQAPILAAIGLNFILFNTVRLVATKIWTETNAVGHDRKQYRK 360
406 llrstlvlpfghvhytvmalpytevsqtlwqlmqymflnsfqgffvailyfcnge 465
361 LAKSTLVLVLFVGVHYIVFVCLPHS-FTGLGWEIRMHCELFNFSGQFFVSIICYCNGE 419
466 vqaelrkswtlaldfkrkarsgs 491
420 VQAEVKMWSRNLSDWKRPCCGS 445

RESULT 5
ID PTHR_HUMAN STANDARD; PRT; 593 AA.
AC Q03431;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR.
GN PTHR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN TISSUE=KIDNEY;
RC TISSUE=KIDNEY;
RX MEDLINE; 93238641.
RA SCHIPANI E., KARGA H., KARAPLIS A.C., POTTS J.T. JR., KRONENBERG H.M.,
RA ABOU-SAMRA A.B.B., SEGRE G.V., JUEPPNER H.;
RL ENDOCRINOLOGY 132:2157-2165(1993).
[2]
RN TISSUE=KIDNEY;
RC TISSUE=KIDNEY;
RX MEDLINE; 93387403.
RA SCHNEIDER H., FEYEN J.-H., RAO MOVVA N.;
RL EUR. J. PHARMACOL. 246:149-155(1993).
[3]
RN TISSUE=KIDNEY;
RC TISSUE=KIDNEY;
RX MEDLINE; 95263723.
RA SCHIPANI E., WEINSTEIN L.S., BERGWITZ C., IIDA-KLEIN A., KONG X.F.,
RA STUHRMANN M., KRUSE K., WHYTE M.P., MURRAY T., SCHMIDTKE J., DOP C.,
RA BRICKMAN A.S., CRAWFORD J.D., POTTS J.T., KRONENBERG H.M.,
RA ABOU-SAMRA A.B., SEGRE G.V., JUEPPNER H.;
RL J. CLIN. ENDOCRINOL. METAB. 80:1611-1621(1995).
[4]
RN TISSUE=KIDNEY;
RC TISSUE=KIDNEY;
RA LEVINE M.A.;
RL SUBMITTED (XXX-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATES ADENYLYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
CC KIDNEY, BONE AND LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L04308; G190722; -.
DR EMBL; X68596; G396813; -.

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DR EMBL; U22409; G897596; -.
DR EMBL; U22401; G897596; JOINED.
DR EMBL; U22402; G897596; JOINED.
DR EMBL; U22403; G897596; JOINED.
DR EMBL; U22404; G897596; JOINED.
DR EMBL; U22405; G897596; JOINED.
DR EMBL; U22406; G897596; JOINED.
DR EMBL; U22407; G897596; JOINED.
DR EMBL; U22408; G897596; JOINED.
DR EMBL; U17418; G596130; -.
DR PIR; S29610; S29610.
DR PIR; A49191; A49191.
DR GCRDB; GCR_0205; -.
DR GCRDB; GCR_0647; -.
DR MTM; 168468; 11TH EDITION
DR PROSITE; PS00649; G-PROTEIN_RECEP_F2_1.
DR PROSITE; PS00650; G-PROTEIN_RECEP_F2_2.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 26
FT CHAIN 27 593 PTH/PTHr RECEPTOR.
FT DOMAIN 27 188 EXTRACELLULAR (POTENTIAL).
FT TRANSNEM 189 212 1 (POTENTIAL).
FT DOMAIN 213 219 CYTOPLASMIC (POTENTIAL).
FT TRANSNEM 220 239 2 (POTENTIAL).
FT DOMAIN 240 282 EXTRACELLULAR (POTENTIAL).
FT TRANSNEM 283 306 3 (POTENTIAL).
FT DOMAIN 307 320 CYTOPLASMIC (POTENTIAL).
FT TRANSNEM 321 342 4 (POTENTIAL).
FT DOMAIN 343 361 EXTRACELLULAR (POTENTIAL).
FT TRANSNEM 362 382 5 (POTENTIAL).
FT DOMAIN 383 409 CYTOPLASMIC (POTENTIAL).
FT TRANSNEM 410 428 6 (POTENTIAL).
FT DOMAIN 429 440 EXTRACELLULAR (POTENTIAL).
FT TRANSNEM 441 463 7 (POTENTIAL).
FT DOMAIN 464 593 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 151 151 POTENTIAL.
FT CARBOHYD 166 166 POTENTIAL.
FT CARBOHYD 176 176 POTENTIAL.
FT CONFLICT 471 471 K -> N (IN REF. 2).
FT CONFLICT 473 473 S -> C (IN REF. 2).
SQ SEQUENCE 593 AA; 66360 MW; 8254CA96 CRC32;

Query Match 47.0%; Score 1942; DB 7; Length 593;
Best Local Similarity 58.8%; Pred. No. 0.00e+00;
Matches 235; Conservative 79; Mismatches 80; Indels 6; Gaps 6;

Db 108 clpewdhilcwpigapgevavpcpdyiydfnhkhghayrrcdngswelyvghnrtwany 167
QY 63 CFPEDWGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 122

Db 168 secvkfltnetr-erevf-drlgmitycvgsvaslsltvavllayfrlhtctnylmh 225
QY 123 SDCLRLQPDISIGKQECERLYVMTYVGYISGSLAVAILIIGYFRLHCTRNHYHM 182

Db 226 lfsfmlraasifvkdavlysgftldeaelrteehhlaqvppppaaavagcgvav 285
QY 183 LFSFMLRATISIFKDRVYVHAHIGVKELESIMOD-DP-QNSIEATSVDKSQYIGCKIAV 240

Db 286 tfflyflatnywllvegilyhslfmaffsekkyllwgtlfgwglpavfvavvgrat 345
QY 241 VMFYFLATNYWLLVEGLYLHNLIFVAFSDTKYLGWFLIIGWGFPAFVAANAVARAT 300

Db 346 lantgcwldssghkwiqvillasvlnfilnirvlatklretnagrcdtrqyrk 405
QY 301 LADARCWELSAGDKIWKIYQAPILAAIGLNFILFNTVRLVATKIWTETNAVGHDRKQYRK 360

Db 406 llrstlvlpfghvhytvmalpytevsqtlwqlmqymflnsfqgffvailyfcnge 465
QY 361 LAKSTLVLVLFVGVHYIVFVCLPHS-FTGLGWEIRMHCELFNFSGQFFVSIICYCNGE 419

Db 466 vqaelrkswtlaldfkrkarsgs 491
QY 420 VQAEVKMWSRNLSDWKRPCCGS 445

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Query Match	22.0%;	Score 907;	DB 9;	Length 437;
Best Local Similarity	38.5%;	Pred. No. 9,38e-162;		

Matches 148; Conservative 101; Mismatches 101; Indels 34; Gaps 22;

Db 37 cael-lssq-tenracsgvwdnltcwradgetvpcpkvfnfysrpniskncts 94
 QY 48 C-ELNITAOLOEGEGNCFPEWDGLICWPGTGVKISAVPCPPYIDFNHK-GVAFRHCNP 105
 Db 95 dg-ws-etfpe-fid-a-c-gyndpe-deskifvylvkaityltgysvslmsttgsii 146
 QY 106 NGTDFMHSLNKWTWANSYDCLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAIL 165
 Db 147 iclfrklhctryihlnflsfmralsvldsvlyssgl--lrc-----hdqp-----a 196
 QY 166 IGYFRRLHCTRYIHMHLEVSFMLRATSFIVKRVVHAHIGVKELESIMQDDPQNSIEA 225
 Db 197 -----s-wgcklsivffgcymanfyllveglvhltil-vailppscflaylligw 249
 QY 226 TSVDKSOYIGCKIAVVMYIYFLATNYIWLVEGLYHNLIFVAFSDTKYLWGFIILGW 285
 Db 250 ipscigawtatrslsdgtcwtndhsipwvrmpllisivnlfalsivrlqlk1 309
 QY 286 FPAFAVAANAVARATLADARCWELSAGDIKW-IYQAPILAAIGLNFILNTVRLATKI 344
 Db 310 -tspdvvgndsqykrakstlllplfgvymvfaafpiggss-tyqi-lf-elcvgsf 365
 QY 345 WETNAVGHDRKQYRKRLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSF 404
 Db 366 qglvavlycflnseqcelkrw 389
 QY 405 QGFFVSIICYNGEVAEKKMW 428

RESULT 11
 ID VIPS RAT STANDARD; PRT; 437 AA.
 AC P35000;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2)
 DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR)
 DE (PACAP TYPE III RECEPTOR) (PACAP-R-3).
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-SPRAGUE-DAWLEY; TISSUE-OLFACTORY BULB;
 RX MEDLINE; 94033806.
 RA LUTZ E.-M., SHEWARD W.J., WEST K.M., MORROW J.A., FINK G.,
 RA HARMAR A.J.;
 RA FEBS LETT. 334:3-8(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CEREBRAL CORTEX;
 RX MEDLINE; 95080140.
 RA USUDIN T.B., BONNER T.I., MEZEY E.;
 RL ENDOCRINOLOGY 135:2662-2680(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE ADENYLATE CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; 225885; G414189; -;
 DR EMBL; U09631; G495196; -;
 DR PIR; S39069; S39069.
 DR GCRDB; GCR_0794; -;
 DR PROSITE; PS00649; G-PROTEIN_RECF_F2_1.
 DR PROSITE; PS00650; G-PROTEIN_RECF_F2_2.
 KW G-PROTEIN COUPLED RECEPTOR; TRNSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 437 VASOACTIVE INTESTINAL POLYPEPTIDE
 FT DOMAIN 23 125 RECEPTOR 2.
 FT TRANSMEM 126 150 EXTRACELLULAR (POTENTIAL).
 FT 1 (POTENTIAL).

DOMAIN 151 157 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 158 177 2 (POTENTIAL).
 DOMAIN 178 202 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 203 226 3 (POTENTIAL).
 DOMAIN 227 239 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 240 261 4 (POTENTIAL).
 DOMAIN 262 278 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 279 302 5 (POTENTIAL).
 DOMAIN 303 327 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 328 347 6 (POTENTIAL).
 DOMAIN 348 359 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 360 379 7 (POTENTIAL).
 DOMAIN 380 437 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 57 57 POTENTIAL.
 CARBOHYD 87 87 POTENTIAL.
 CARBOHYD 91 91 POTENTIAL.
 FT CONFLICT 383 383 C -> R (IN REF. 2)
 SQ SEQUENCE 437 AA; 49552 MW; 88736A73 CRC32;

Query Match 21.8%; Score 900; DB 9; Length 437;
 Best Local Similarity 38.0%; Pred. No. 3.14e-160;
 Matches 146; Conservative 101; Mismatches 103; Indels 34; Gaps 22;

Db 37 cael-lssq-tenracsgvwdnltcwradgetvpcpkvfnfysrpniskncts 94
 QY 48 C-ELNITAOLOEGEGNCFPEWDGLICWPGTGVKISAVPCPPYIDFNHK-GVAFRHCNP 105
 Db 95 dg-ws-etfpe-fid-a-c-gyndpe-deskifvylvkaityltgysvslmsttgsii 146
 QY 106 NGTDFMHSLNKWTWANSYDCLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAIL 165
 Db 147 iclfrklhctryihlnflsfmralsvldsvlyssgl--lrc-----hdqp----- 195
 QY 166 IGYFRRLHCTRYIHMHLEVSFMLRATSFIVKRVVHAHIGVKELESIMQDDPQNSIEA 225
 Db 196 -g--s-wgcklsivffgcymanfyllveglvhltil-vailppscflaylligw 249
 QY 226 TSVDKSOYIGCKIAVVMYIYFLATNYIWLVEGLYHNLIFVAFSDTKYLWGFIILGW 285
 Db 250 ipscigawtatrslsdgtcwtndhsipwvrmpllisivnlfalsivrlqlk1 309
 QY 286 FPAFAVAANAVARATLADARCWELSAGDIKW-IYQAPILAAIGLNFILNTVRLATKI 344
 Db 310 -tspdvvgndsqykrakstlllplfgvymvfaafpiggss-tyqi-lf-elcvgsf 365
 QY 345 WETNAVGHDRKQYRKRLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSF 404
 Db 366 qglvavlycflnseqcelkrw 389
 QY 405 QGFFVSIICYNGEVAEKKMW 428

RESULT 12
 ID VIPS HUMAN STANDARD; PRT; 438 AA.
 AC P41587;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2)
 DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR)
 DE (PACAP TYPE III RECEPTOR) (PACAP-R-3) (HELODERMIN-PREFERRING VIP RECEPTOR).
 GN VIPR2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95110300.
 RA SVOBODA M., TASTENOY M., VAN RAMPENBERGH J., GOOSENS J.F., NEEF P.,
 RA WAELEBROECK M., ROBBERECHT P.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1617-1624(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,

Db 299 -rnsnmnyllirpblfaigvnlvflrviciviaki-kanlmcktdik-cr-lakstl 354
 QY 309 LSAGDIK-W-IYQAPILAAIGLNFLELNTVRLATKIWEINAVGHDTRKQYRKLAKSTL 366
 Db 355 tlipllgthevifavmdehargtlrf-vkltfsltsfsgfmavlycfvnnvqmef 413
 QY 367 VLVLVEGVHYIVFV-CLP-HSFTGLGWELIRHCELFNFSSFGQFFVSIICYCNGEVOAEV 424
 Db 414 rkswerwrl 422
 QY 425 KRWRSRWNL 433

RESULT 14
 ID GLR_HUMAN STANDARD; PRT; 477 AA.
 AC P47871;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE GLUCAGON RECEPTOR PRECURSOR (GL-R).
 GN GCGR. (HUMAN).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE; 94121651.
 RA MACNEIL D.J., OCCI J.L., HEY P.J., STRADER C.D., GRAZIANO M.P.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 198:328-334(1994).
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94192999.
 RA LOK S., KUIJPER J.L., JELINEK L.J., KRAMER J.M., WHITMORE T.E.,
 RA SPRECHER C.A., MATHWES S., GRANT F.J., BIGGS S.H., ROSENBERG G.B.;
 RL GENE 140:203-209(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON. THE ACTIVITY OF THIS
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 SYSTEM.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U03469; G439690; -.
 DR EMBL; L20316; G405190; -.
 DR MIM; 138033; 11TH EDITION.
 CC G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 ?
 FT CHAIN ? 477
 FT DOMAIN ? 142
 FT TRANSMEM 143 166
 FT DOMAIN 167 173
 FT TRANSMEM 174 193
 FT DOMAIN 194 225
 FT TRANSMEM 226 249
 FT DOMAIN 250 263
 FT TRANSMEM 264 285
 FT DOMAIN 286 303
 FT TRANSMEM 304 326
 FT DOMAIN 327 350
 FT TRANSMEM 351 369
 FT DOMAIN 370 381
 FT TRANSMEM 382 404
 FT DOMAIN 405 477
 FT CARBOHYD 46 46
 FT CARBOHYD 59 59
 FT CARBOHYD 74 74
 FT CARBOHYD 78 78
 SQ SEQUENCE 477 AA; 54009 MW; DB3FF092 CRC32;

Query Match 20.5%; Score 845; DB 4; Length 477;
 Best Local Similarity 34.4%; Pred. No. 2.84e-148;
 Matches 137; Conservative 102; Mismatches 138; Indels 21; Gaps 17;

Db 42 qchhnlslppptelvcnrtfdkyscwpdtpanttaniscpwyplwhhkvqhrfvfkrcg 101
 QY 47 QCELNITIAQLQEGEGNGCFPEWDGLICWPRTVGKISAVPCPPYI-YDFN-HKGVAFFHCN 104
 Db 102 pdgqw-vrgprgprwdasqc-qmdgeeelevqvakmysfgvmytvgyslslgalla 159
 QY 105 PNGTWDPMHSLNKTWANSQCLRFLOPDISIGKQ-E-FCERLYVMYTVGYISFGSLAVA 162
 Db 160 lallgglslhctnaihlanfasfvkassvivdgllltrysqk-----i-gdd-l-s 211
 QY 163 ILIIGYFRRLECHTRNYIHMHLFVSMRLATSIIFKRVKRVVHAHIGVKELESLIMQDDPONS 222
 Db 212 v-stwlsdgvagcrrvaavfmqygiavnycwlliveglylhnllqlatlpersffslylgi 270
 QY 223 IEATSDVKSOYIGCKIAVMFIYFLATNYIWLVEGYLHNLIFVAFFSDTKLWGFILI 282
 Db 271 gwgapmlfvvypavvkcelfenvqgwtensdmqfwllrfpflailnffivrlqvlv 330
 QY 283 GWGPPAAFAVAVARATLADARCWELSAG-DIKWIIYQAPILAAIGLNFLELNTVRLA 341
 Db 331 akr-arqmhbtdyk-fr-lakstltlpllgvhevfvafvtdehaqgtlrsaklffdlf 387
 QY 342 TKIWTWNAVGHDRKQYRKLAKSTLVLVYGVHYIYFVCLPHSFT-GLGWELRMHCELF 400
 Db 388 lssfgllvavlycflnkvqselrrrrwhrwlqkvlw 425
 QY 401 FNSFQGFVSIICYCNGEVOAEVKKMSRWNL-SVDW 437

RESULT 15
 ID GLR_RAT STANDARD; PRT; 485 AA.
 AC P30082;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE GLUCAGON RECEPTOR PRECURSOR (GL-R).
 GN GCGR.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93206096.
 RA JELINEK L.J., LOK S., GRANT F.J., ROSENBERG G.B., SMITH R.A.,
 RA BENSCHE P.A., SHEPPARD P.O., O'HARA P.J., FOSTER D.C.,
 RA KUIJPER J.L., BIGGS S.H., WALKER K.M., CHEN L.H., MCKERNAN P.A.,
 RA KINDSVOGEL W.;
 RA SCIENCE 259:1614-1616(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93213282.
 RA SVOBODA M., CICCARELLI E., TASTENOY M., CAUVIN A., STIEVENART M.,
 RA CHRISTOPHE J.;
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE=LIVER;
 RX MEDLINE; 94364484.
 RA MAGET B., TASTENOY M., SVOBODA M.;
 RL FEBS LETT. 351:271-275(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON. THE ACTIVITY OF THIS
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 SYSTEM.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; L04796; G457614; -.
 DR EMBL; X68692; G463258; -.
 DR EMBL; M96674; G204374; -.
 DR EMBL; L31574; G473766; -.
 DR PIR; S29689; S29689.
 DR PIR; JQ1957; JQ1957.
 DR GCRDB; GCR_0539; -.

DR GCRDB; GCR_0540; -
 DR GCRDB; GCR_0657; -
 DR PROSITE; PS00649; G-PROTEIN_RECP_F2.1.
 DR PROSITE; PS00650; G-PROTEIN_RECP_F2.2.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 ?

FT CHAIN 1 ?
 FT DOMAIN 7 485 GLUCAGON RECEPTOR.
 FT DOMAIN 143 143 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 144 167 1 (POTENTIAL).
 FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 175 194 2 (POTENTIAL).
 FT DOMAIN 195 226 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 227 250 3 (POTENTIAL).
 FT DOMAIN 251 264 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 265 286 4 (POTENTIAL).
 FT DOMAIN 287 304 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 305 327 5 (POTENTIAL).
 FT DOMAIN 328 351 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 352 370 6 (POTENTIAL).
 FT DOMAIN 371 382 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 383 405 7 (POTENTIAL).
 FT DOMAIN 406 485 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 60 60 POTENTIAL.
 FT CARBOHYD 75 75 POTENTIAL.
 FT CARBOHYD 79 79 POTENTIAL.
 FT CONFLICT 216 216 W -> C (IN REF. 2).
 FT CONFLICT 324 324 V -> A (IN REF. 2).
 SQ SEQUENCE 485 AA; 55038 MW; 05D9BFDC CRC32;

Query Match 20.5%; Score 845; DB 4; Length 485;
 Best Local Similarity 34.0%; Pred. No. 2.84e-148;
 Matches 133; Conservative 101; Mismatches 137; Indels 20; Gaps 15;

Db 43 qchhslslppptelvcnrtfdkyscwtdpnttaniscpwykqhvqhrly-fkrc 101
 QY 47 QCELNITAOQEKGNCFFPEWDGLICWPRGTGKISAVPCPPYI--YD-FNHKGVAFRHC 103
 Db 102 gpdqgw-vrgprgqswdasqcmdddelevqkvakmyssygmvytgysslsqallla 160
 QY 104 NPNGTWDFMHSLNKTNWANSYC-LRFLQPDISIGKEFCERLYVMYTVGYISFGSLAVA 162
 Db 161 lvllglrlxhctryihgnlfasvfkagsvldwidlktrysqk-----l-gdd-l-s 212
 QY 163 ILIIGYERLHCTRYIHMLFVSEMLRATSFVKDRVVHAHIGVKELESIMQDDPQNS 222
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 QY 401 FNSFOGFVSIICYCNGEVAEKKMSRW 431

Search completed: Thu Feb 6 12:25:48 1997
 Job time : 27 secs.

100



 W P S R E H

 (TM)

Release 2.1b John F. Collins, Biocomputing Research Unit.
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MPSrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
 Run on: Fri Feb 7 09:05:06 1997; MasPar time 1411.58 Seconds
 Tabular output not generated. 1168.691 Million cell updates/sec

File: >US-08-468-011-1
 Description: (1-2003) from US08468011.seq (1 of 2)
 Perfect Score: 2003
 N.A. Sequence: 1 GTTTGCTCTGGGACGCAAG.....ATTGCTCTGTGATTGTCA 2003
 Comp: CAACAGAGACCCGTCGGTTC.....TAACGAGACACTAACAGT

Scoring table: TABLE default
 Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-new5

1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI
 10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank94

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7
 23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5
 30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2
 37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2
 44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1
 51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8
 58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1
 64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8
 71:SVR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4
 78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database: genbank-news

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG
 89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database: u-emb146_94

96:part1

Statistics: Mean 11.914; Variance 4.178; scale 2.851

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1950	97.4	2641	9	Human PTH2 parathyroid	0.00e+00
2	1950	97.4	2641	56	Human PTH2 parathyroid	0.00e+00
3	626	31.3	1980	90	Human parathyroid hor	0.00e+00

4	626	31.3	1980	9	HSTHR05	Human parathyroid hor	0.00e+00
5	269	13.4	1878	33	OPOTHR	Opossum parathyroid h	7.57e-270
6	256	12.8	2067	34	SSU18315	Sus scrofa parathyroi	1.86e-254
7	253	12.6	1836	69	RATPTHRR	Rat parathyroid hormo	6.53e-251
8	253	12.6	2065	69	RATPTHRR	Rat parathyroid hormo	6.53e-251
9	246	12.3	1984	64	MMPHRPR	M.musculus mRNA for p	1.21e-242
10	242	12.1	1948	60	HUMPTRH	Human parathyroid hor	6.33e-238
11	240	12.0	2095	55	HSPHR	H.sapiens mRNA for pa	1.44e-235
12	240	12.0	2171	56	HSU17418	Human parathyroid hor	1.44e-235
13	140	7.0	548	90	HSTHR03	Human parathyroid hor	1.94e-119
14	140	7.0	548	9	HSTHR03	Human parathyroid hor	1.94e-119
15	104	5.2	744	90	HSU47124	Human parathyroid hor	4.21e-79
16	104	5.2	744	9	HSU47124	Human parathyroid hor	4.21e-79
17	95	4.7	95	9	HSTHR02	Human parathyroid hor	3.01e-69
18	95	4.7	95	90	HSTHR02	Human parathyroid hor	3.01e-69
19	74	3.7	1003	55	HSTHPRH5	Human parathyroid hor	8.38e-47
20	71	3.5	641	90	HSTHR01	Human parathyroid hor	1.12e-43
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22	67	3.3	154	69	RATPTHYRH	Rat parathyroid hormo	1.50e-39
23	64	3.2	1766	67	MUSPTHRO5	Mus musculus parathyr	1.74e-36
24	61	3.0	1849	62	S79852	glucose-dependent ins	1.87e-33
25	61	3.0	2025	56	HSU32331	Human GIP receptor (G	1.87e-33
26	61	3.0	2181	53	HSGDIPR	H.sapiens mRNA for g1	1.87e-33
27	58	2.9	1616	56	HSU13989	Human secretin recept	1.86e-30
28	58	2.9	1650	56	HSU20178	Human secretin recept	1.86e-30
29	58	2.9	1703	56	HSU28281	Human secretin recept	1.86e-30
30	59	2.9	2785	63	CRUGIPR	Hamster mRNA for GIP	1.88e-31
31	57	2.8	2116	70	S75952	glucagon-like peptide	1.83e-29
32	57	2.8	3066	68	RATGLIRCP	Rat mRNA sequence.	1.83e-29
33	52	2.6	2348	61	HUMVAIPR	Homo sapiens vasoacti	1.41e-24
34	52	2.6	2684	56	HSVIPRE	H.sapiens HIVR mRNA f	1.41e-24
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37	52	2.6	2834	56	HSVIPRRP	H.sapiens intestinal	1.41e-24
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45	49	2.4	2599	69	RATPACAP2	Rat mRNA for rat PACA	1.05e-21

ALIGNMENTS

RESULT 1
 ID H251281 standard; RNA; PRI; 2641 BP.
 AC U25128;
 DT 08-JUL-1995 (Rel. 44, Created)
 DT 09-APR-1996 (Rel. 47, Last updated, Version 3)
 DE Human PTH2 parathyroid hormone receptor mRNA, complete cds.
 KW
 OS Homo sapiens (human)
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homidae.
 RN [1]
 RP 1-2641
 RX MEDLINE; 95318121.
 RA Usdin T.B., Gruber C., Bonner T.I.;
 RT "Identification and functional expression of a receptor
 selectively recognizing parathyroid hormone, the PTH2 receptor";
 RL J. Biol. Chem. 270:15455-15458(1995).
 RN [2]
 RP 1-2641
 RA Bonner T.I.;
 RT ;
 RL Submitted (17-APR-1995) to the EMBL/GenBank/DBJ databases.
 RL Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg. 36, Room 3A-17,
 DR Bethesda, MD 20892-4090, USA
 CC SWISS-PROT; P49190; PTR2_HUMAN.
 CC NCBI gi: 887966 Location/Qualifiers
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NID g164288
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SOURCE Didelphis virginiana kidney cDNA to mRNA.
ORGANISM Didelphis virginiana
REFERENCE 1 (bases 1 to 1878)
AUTHORS Juppner,H., Abou-Samra,A.-B.B., Freeman,M.W., Kong,X.F.,
Schropani,E., Richards,J., Kolakowski,L.F., Jr., Hock,J., Potts,J.T.,
Kronenberg,H.M. and Segre,G.
TITLE A G-protein linked receptor for parathyroid hormone related peptide
JOURNAL Science 254, 1024-1026 (1991)
MEDLINE 92054592
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AUTHORS	1 (bases 1 to 2095)		
TITLE	Schneider,H.		
JOURNAL	Direct Submission		
REMARK	Submitted (02-OCT-1992) to the EMBL/GenBank/DBJ databases. H.		
REFERENCE	Schneider, Preclinical Research, Sandoz Pharma AG, Bau 386 / 322, CH- 4002 Basel, SWITZERLAND		
AUTHORS	sequence revised by author (17-AUG-1993)		
TITLE	2 (bases 1 to 2095)		
JOURNAL	Schneider,H., Feyen,J.H., Seuwen,K. and Movva,N.R.		
MEDLINE	Cloning and functional expression of a human parathyroid hormone receptor		
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DEFINITION Human parathyroid hormone receptor 2 (PTH2) gene, exon 2, partial cds.
ACCESSION U47124
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KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Usdin,T.B., Gruber,C. and Bonner,T.I.
TITLE Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor
JOURNAL J. Biol. Chem. 270 (26), 15455-15458 (1995)
MEDLINE 95318121
REFERENCE 2 (bases 1 to 744)
AUTHORS Usdin,T.B., Modi,W. and Bonner,T.I.
TITLE Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33 by fluorescence in situ hybridization
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 744)
AUTHORS Bonner,T.I. and Usdin,T.B.
TITLE Direct Submission
JOURNAL Submitted (02-APR-1996) Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg. 36, Rm 3A17, MSC 4090, Bethesda, MD 20892-4090, USA
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Db 120 aaagtacaatggaactcaacatcacagctcaactcagggaggag 165
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Qy 222 AAAGTACATGTGAATCAACATCAACATCAGCTCACTCCAGGAGGAG 267
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